

Web Table G: Late genes.

Cell cycle regulation		
<i>wee1</i>	SPCC18B5.03	mitosis inhibitor protein kinase; negatively regulates G2/M transition
<i>srw1 ste9</i>	SPAC144.13C	APC regulator, <i>CDC20/fizzy</i> family; required for conjugation
	SPBP8B7.27	putative ubiquitin-protein ligase, HECT domain
	SPBC14F5.10C	RING domain protein, possible E3 ubiquitin ligase
Cell wall		
	SPAC23H3.11C	putative beta-glucan synthesis-associated protein
	SPBC11C11.05	putative cell-wall synthesis protein
<i>mok12</i>	SPBC32H8.13C	alpha glucan synthase
cAMP pathway		
<i>git1</i>	SPBC215.04	G gamma subunit of the <i>gpa2/git5/git1</i> heterotrimeric G protein
<i>cgs1</i>	SPAC8C9.03	cAMP-dependent protein kinase regulatory chain; similar to <i>S. cerevisiae BCY1</i>
<i>pkal git6</i>	SPC110.10	cAMP-dependent protein kinase catalytic subunit
<i>git3</i>	SPCC1753.02C	adenylate cyclase activation protein
Transcription		
	SPBC1105.14	putative zinc-finger transcriptional activator for genes involved in the multistress response by similarity to <i>S. cerevisiae MSN2</i> (also in stress group)
	SPCC1919.14C	putative transcription factor <i>tffiib</i> component
	SPBC25B2.03	putative zinc finger protein
DNA repair		
<i>rhp16</i>	SPCC330.01C	nucleotide excision repair protein; <i>SNF2</i> type DNA helicase; similar to <i>S. cerevisiae RAD16</i>
	SPAC2F7.06C	DNA polymerase X family; involved in repair
<i>rad17</i>	SPCC330.02	dna repair protein, nucleotide excision repair, <i>S. cerevisiae RAD7</i> homolog
<i>uve1</i>	SPBC19C7.09C	UV-endonuclease.
Stress		
<i>mpr1 spy1</i>	SPBC725.02	stress response regulator phosphotransmitter; response regulator phosphotransferase; similar to <i>S. cerevisiae YPD1</i>
<i>ptc4</i>	SPAC4A8.03C	protein phosphatase 2C isoform
	SPAC688.04C	glutathione S transferase 3
<i>cta1</i>	SPCC757.07C	catalase
<i>rds1</i>	SPAC343.12	stress response protein <i>rds1p</i>
	SPBC1105.14	putative zinc-finger transcriptional activator for genes involved in the multistress response by similarity to <i>S. cerevisiae MSN2</i>
Mitochondrial genes		
	P05501	mitochondrial-cytochrome b
	P05511	mitochondrial-hypothetical 91 KDa protein in <i>cob</i> intron
	P07657	mitochondrial-cytochrome C oxidase polypeptide I (EC 1.9.3.1).
	P14575	mitochondrial- cytochrome C oxidase polypeptide III (EC 1.9.3.1).
	P21535	mitochondrial-ATP synthase A chain precursor (EC 3.6.3.14) (protein 6).
	P21536	mitochondrial-ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
	P21537	mitochondrial-ATP synthase protein 9, mitochondrial (EC 3.6.3.14) (lipid-binding protein).
	P21547	mitochondrial-hypothetical 25.5 KDa protein in ATP6-ATP8 intergenic region (<i>urfA</i>).
	P22191	mitochondrial-hypothetical <i>cox1</i> intron-1 45.6 Kda protein (probable maturase).
Metabolic		
	SPAC869.08	putative protein-l-isoaspartate o-methyltransferase
	SPAC750.02C	putative membrane transporter
	SPAC13A11.06	putative pyruvate decarboxylase (EC 4.1.1.1)
	SPCC663.07C	short chain dehydrogenase pseudogene
	SPBC1198.01	putative glutathione-dependent formaldehyde dehydrogenase
	SPCC1281.07C	protein with Glutathione S transferase domain

	SPAPB1A11.03	putative FMN dependent dehydrogenase; similar to lactate dehydrogenase
	SPAC186.02C	2-hydroxyacid dehydrogenase homolog
	SPCC663.13C	putative acetyltransferase; similar to <i>S. cerevisiae</i> YOR253W
	SPCC1450.13C	riboflavin synthase alpha chain
	SPAP27G11.09C	putative gtp cyclohydrolase; possible riboflavin biosynthesis
	SPAC1002.19	putative GTP cyclohydrolase; riboflavin biosynthesis
	SPCC1281.04	pyridoxal reductase homolog
	SPAC869.07C	putative alpha-galactosidase
<i>gmh1</i>	SPAC5H10.11	putative galactosyltransferase; high similarity to Gmh3p, which is an alpha-1,2-galactosyltransferase
<i>gna1</i>	SPAC16E8.03	acetyltransferase involved in UDP-N-acetylglucosamine synthesis
	SPAC513.02	protein with similarity to phosphoglycerate mutases
	SPAC4H3.08	putative short chain dehydrogenase
	SPAC22A12.17C	short chain dehydrogenase; possible sorbitol utilization
	SPBC1773.06C	alcohol dehydrogenase
	SPAC2E1P3.01	putative dehydrogenase by similarity
	SPAC23D3.05C	alcohol dehydrogenase pseudogene
	SPAC139.05	probable succinate semialdehyde dehydrogenase
<i>tms1</i>	SPBC1773.05C	putative sorbitol dehydrogenase
	SPACUNK4.17	putative sugar oxidoreductase; possible sorbitol utilisation
	SPBC24C6.09C	similarity to transketolase; Pfam-B_53149; Pfam-B_17168
Orphans		
	SPCC1235.03	hypothetical protein; sequence orphan
	SPAC15F9.01C	hypothetical protein; sequence orphan
	SPAC15A10.07	hypothetical protein; sequence orphan
	SPCC24B10.16C	hypothetical protein; sequence orphan; has transcript on microarray
	SPAC32A11.02C	hypothetical protein; sequence orphan; contains predicted coiled-coil region
	SPAPB8E5.10	hypothetical protein; sequence orphan; similarity (low) to <i>Drosophilla</i> CG12569
	SPAC23H3.04	hypothetical protein; similar to <i>S. pombe</i> SPAC1952.10C; possible <i>S. pombe</i> specific protein
	SPBC3H7.08C	hypothetical protein; sequence orphan
	SPBC685.03	hypothetical serine-rich protein; sequence orphan; predicted N-term signal sequence
	SPAPB1A10.08	hypothetical protein.; sequence orphan
	SPBC409.17C	hypothetical protein; sequence orphan
	SPBC17D1.01	hypothetical protein; sequence orphan
	SPAC4F10.17	hypothetical protein; sequence orphan; predicted N-terminal signal sequence
	SPCC1494.03	hypothetical protein; sequence orphan
	SPCC1682.06	hypothetical protein; 2 predicted transmembrane helices; Pfam-B_23431; similar to <i>S. pombe</i> SPBC18H10.18C; possibly <i>S. pombe</i> specific
	SPAC18G6.09C	hypothetical serine-rich protein; sequence orphan
	SPCC16A11.15C	hypothetical protein; sequence orphan
	SPAC343.20	hypothetical protein; sequence orphan; has transcript profile on microarray
	SPBPB2B2.19C	hypothetical protein; duplicated at telomere; almost identical to SPAC1348.02 and SPAC756.05; 5 predicted transmembrane helices; possibly <i>S. pombe</i> specific
	SPCC569.03	hypothetical repeat containing protein; see also SPCC569.01 SPCC613.11C; SPBC106.08C; SPCC330.04C; possibly <i>S. pombe</i> specific
	SPCC736.05	hypothetical wtf-like protein; <i>S. pombe</i> -specific
	SPBP4G3.03	hypothetical protein; possibly <i>S. pombe</i> specific; similar at the N-term to SPBP7G5.01
	SPAC1348.02	hypothetical protein; 5 predicted transmembrane helix; low similarity to membrane transporter; highly similar to SPBPB2B2.19C SPAC750.05C SPAC977.01; possibly <i>S. pombe</i> specific
	SPAC977.01	hypothetical protein; possibly <i>S. pombe</i> specific; telomeric duplication; highly similar to <i>S. pombe</i> SPAC750.05C SPAC1348.02 and SPBPB2B2.19C
	SPAC750.05C	hypothetical protein; low similarity to <i>S. cerevisiae</i> YHL017W is probably spurious; highly similar to <i>S. pombe</i> SPAC1348.02; highly similar to <i>S. pombe</i> SPBPB2B2.19c; possibly <i>S.</i>

		<i>pombe</i> specific
	SPBC18H10.18C	hypothetical protein; 2 predicted transmembrane helices; very high similarity to SPCC1682.06; possibly <i>S. pombe</i> specific
	SPAC15E1.10	hypothetical protein; possibly <i>S. pombe</i> specific; similar to SPBP4G3.03
	SPCC737.04	hypothetical protein; possibly <i>S. pombe</i> specific
	SPAC14C4.01C	hypothetical protein; sequence orphan
	SPAC23H3.15C	hypothetical serine-rich protein; sequence orphan
	SPCC1393.12	hypothetical protein; sequence orphan
	SPAC15E1.02C	hypothetical protein; sequence orphan; 3 predicted transmembrane helices
	SPCC191.01	hypothetical protein; sequence orphan
Others		
	cosmid SPAC1D4	cDNA, no corresponding ORF could be predicted; misc RNA 2.2.20.RC
	SPAC11D3.13	conserved hypothetical protein; ThiJ domain
	SPAP14E8.05C	conserved hypothetical protein; 3 predicted transmembrane helices
	SPAC1F7.06	conserved hypothetical protein
	SPCC663.14C	hypothetical protein; similar to <i>S. cerevisiae</i> YPL221W; predicted N-terminal signal sequence; 8 predicted transmembrane helices
	SPBC1685.14C	hypothetical protein; similar to <i>S. cerevisiae</i> YNL212W
	SPCC16A11.01	hypothetical protein; similar to <i>S. cerevisiae</i> YKL051W
	SPCC1322.03	hypothetical protein; similar to <i>S. cerevisiae</i> YAL053W; 11 predicted transmembrane helices
	SPCC830.08C	hypothetical protein; similar to <i>S. cerevisiae</i> YIP2; possibly involved in membrane trafficking by similarity
	SPBC947.09	hypothetical protein; similar to <i>S. cerevisiae</i> YPL280W; possibly fungal specific
	SPAC23C11.06C	hypothetical protein; similar to <i>S. cerevisiae</i> YNL115C; 5 predicted transmembrane helices
	SPBC21C3.19	hypothetical protein; similar to <i>S. cerevisiae</i> YHR087W
	SPCC4G3.03	hypothetical protein similar to <i>S. cerevisiae</i> YLR149C; putative apoptotic protease activating factor, by low similarity to human spaf1 (conserved catalytic residues)
	SPBC725.03	hypothetical protein; similar to <i>S. cerevisiae</i> YGR017W
	SPBC6B1.03C	hypothetical protein; similar to <i>S. cerevisiae</i> YHR097C
	SPAC16E8.02	hypothetical protein; similar to <i>S. cerevisiae</i> YGL010W; 4 predicted transmembrane helices
	SPAC3C7.02C	hypothetical protein; similar to <i>S. cerevisiae</i> YPL004C
	SPCC970.02	hypothetical protein; similar to <i>S. cerevisiae</i> YKL046C
	SPAC5H10.02C	hypothetical protein; similar to <i>S. cerevisiae</i> YPL280W
	SPCC757.03C	conserved hypothetical protein
	SPBC20F10.03	hypothetical protein; Pfam-B_11425; similarity to mouse and rat interferon-related developmental regulator 1- nerve growth factor; also conserved in <i>C. elegans</i>
	SPCC1742.01 SPCC1795.13	hypothetical protein; sequence orphan; large repeated threonine-rich region; 4 Tryp_mucin, Mucin-like glycoprotein repeat; predicted N-terminal signal sequence
	SPCC594.04C	hypothetical protein; low similarity to a region of <i>S. cerevisiae</i> Farnesyl cysteine:carboxyl methyltransferase; conserved residues G{VL}{FW}.{WY}SRHPN{FY}{FL}{GA}{E}
	SPAC869.09	hypothetical protein; similar to <i>N. crassa</i> conidiation protein 6
	SPAC22G7.11C SPAC4G8.01C	hypothetical protein; similar to <i>N. crassa</i> conidiation -specific protein 6
	SPAC11D3.01C	protein with similarity to neurospora conidiation specific protein
	SPCC757.02C	hypothetical protein; conserved in <i>A. thaliana</i> ; Pfam-B_37808 domain
	SPAC869.06C	hypothetical protein; low similarity to <i>S. coelicolor</i> SC9H11.25C
	SPAC3G6.07	very hypothetical protein
	SPBC11C11.12	hypothetical protein
	SPBC3D6.01	
	SPBP19A11.02C	putative membrane glycoprotein; predicted N-term signal sequence
	SPBP4H10.10	membrane protein of unknown function, possibly involved in respiration by similarity to YGR101W; rhomboid family
	SPAC328.04	AAA family ATPase with similarity to katanin; putative microtubule severing protein by

		similarity
<i>cmk1</i>	SPACUNK12.02C	calmodulin kinase i homolog
	SPAC22G7.08	putative serine/threonine protein kinase
	SPBC725.06C	putative serine/threonine protein kinase
	SPBC21.07C	putative serine/threonine protein kinase
<i>rga5</i>	SPBC17F3.01C	RhoGAP GTPase activating protein
<i>n150</i>	SPAC31G5.12C	similar to <i>S. cerevisiae</i> <i>MAF1</i> ; putative nuclear-cytoplasmic transport
	SPAC3H8.09C	putative RNA-binding protein
	SPBC2G2.17C	sun family protein; <i>S. cerevisiae</i> homolog involved in aging process and cell cycle regulation
	SPBC1711.12	putative dipeptidyl peptidase; possibly secreted
	SPAC227.01C	potential Protein required for retention of luminal ER proteins; similar to <i>S. cerevisiae</i> <i>ERD1</i>
	SPBC609.01	hypothetical protein; ribonuclease II (RNB) family
	SPBC1685.05	putative serine protease
	SPAC4H3.03C	putative family 15 glycosyl hydrolase
<i>agl</i>	SPAPB24D3.10C	alpha-glucosidase; family 31 glycosyl hydrolase
<i>cmd1</i>	SPBC12D12.02C	DNA polymerase delta subunit
<i>sco1</i>	SPBC119.06	putative cytochrome C oxidase assembly protein